



SEQUENCE LISTING

<110> YOSHINAGA, STEVEN KIYOSHI

<120> POLYPEPTIDES INVOLVED IN IMMUNE RESPONSE

<130> A-579B

<140> US 09/890,729

<141> 2001-08-03

<150> PCT US00/01871

<151> 2000-01-27

<150> 09/264,527

<151> 1999-03-08

<150> 09/244,448

<151> 1999-02-03

<160> 37

<170> PatentIn version 3.2

<210> 1

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<212> DNA

<213> Mus musculus

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<221> CDS

<222> (1)..(600)

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Met	Lys	Pro	Tyr	Phe	Cys	Arg	Val	Phe	Val	Phe	Cys	Phe	Leu	Ile	Arg	
1				5					10					15		

ctt	tta	aca	gga	gaa	atc	aat	ggc	tgc	gcc	gat	cat	agg	atg	ttt	tca	96
Leu	Leu	Thr	Gly	Glu	Ile	Asn	Gly	Ser	Ala	Asp	His	Arg	Met	Phe	Ser	
			20					25					30			

ttt	cac	aat	gga	ggc	gta	cag	att	tct	tgt	aaa	tac	cct	gag	act	gtc	144
Phe	His	Asn	Gly	Gly	Val	Gln	Ile	Ser	Cys	Lys	Tyr	Pro	Glu	Thr	Val	
		35				40						45				

cag	cag	tta	aaa	atg	cga	ttg	ttc	aga	gag	aga	gaa	gtc	ctc	tgc	gaa	192
Gln	Gln	Leu	Lys	Met	Arg	Leu	Phe	Arg	Glu	Arg	Glu	Val	Leu	Cys	Glu	
	50					55					60					

ctc	acc	aag	acc	aag	gga	agc	gga	aat	gcg	gtg	tcc	atc	aag	aat	cca	240
Leu	Thr	Lys	Thr	Lys	Gly	Ser	Gly	Asn	Ala	Val	Ser	Ile	Lys	Asn	Pro	
65					70				75					80		

atg	ctc	tgt	cta	tat	cat	ctg	tca	aac	aac	agc	gtc	tct	ttt	ttc	cta	288
Met	Leu	Cys	Leu	Tyr	His	Leu	Ser	Asn	Asn	Ser	Val	Ser	Phe	Phe	Leu	
			85						90					95		

aac	aac	cca	gac	agc	tcc	cag	gga	agc	tat	tac	ttc	tgc	agc	ctg	tcc	336
Asn	Asn	Pro	Asp	Ser	Ser	Gln	Gly	Ser	Tyr	Tyr	Phe	Cys	Ser	Leu	Ser	
			100					105						110		

att	ttt	gac	cca	cct	cct	ttt	caa	gaa	agg	aac	ctt	agt	gga	gga	tat	384
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Ile	Phe	Asp	Pro	Pro	Pro	Phe	Gln	Glu	Arg	Asn	Leu	Ser	Gly	Gly	Tyr		
		115					120					125					
ttg	cat	att	tat	gaa	tcc	cag	ctc	tgc	tgc	cag	ctg	aag	ctc	tgg	cta		432
Leu	His	Ile	Tyr	Glu	Ser	Gln	Leu	Cys	Cys	Gln	Leu	Lys	Leu	Trp	Leu		
		130				135					140						
ccc	gta	ggg	tgt	gca	gct	ttc	gtt	gtg	gta	ctc	ctt	ttt	gga	tgc	ata		480
Pro	Val	Gly	Cys	Ala	Ala	Phe	Val	Val	Val	Leu	Leu	Phe	Gly	Cys	Ile		
		145			150					155					160		
ctt	atc	atc	tgg	ttt	tca	aaa	aag	aaa	tac	gga	tcc	agt	gtg	cat	gac		528
Leu	Ile	Ile	Trp	Phe	Ser	Lys	Lys	Lys	Tyr	Gly	Ser	Ser	Val	His	Asp		
				165					170					175			
cct	aat	agt	gaa	tac	atg	ttc	atg	gcg	gca	gtc	aac	aca	aac	aaa	aag		576
Pro	Asn	Ser	Glu	Tyr	Met	Phe	Met	Ala	Ala	Val	Asn	Thr	Asn	Lys	Lys		
			180					185					190				
tct	aga	ctt	gca	ggt	gtg	acc	tca										600
Ser	Arg	Leu	Ala	Gly	Val	Thr	Ser										
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 <400> 2

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Phe	His	Asn	Gly	Gly	Val	Gln	Ile	Ser	Cys	Lys	Tyr	Pro	Glu	Thr	Val		
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Gln	Gln	Leu	Lys	Met	Arg	Leu	Phe	Arg	Glu	Arg	Glu	Val	Leu	Cys	Glu		
		50				55					60						
Leu	Thr	Lys	Thr	Lys	Gly	Ser	Gly	Asn	Ala	Val	Ser	Ile	Lys	Asn	Pro		
65					70					75					80		
Met	Leu	Cys	Leu	Tyr	His	Leu	Ser	Asn	Asn	Ser	Val	Ser	Phe	Phe	Leu		
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Asn	Asn	Pro	Asp	Ser	Ser	Gln	Gly	Ser	Tyr	Tyr	Phe	Cys	Ser	Leu	Ser		
			100					105					110				
Ile	Phe	Asp	Pro	Pro	Pro	Phe	Gln	Glu	Arg	Asn	Leu	Ser	Gly	Gly	Tyr		
		115					120					125					
Leu	His	Ile	Tyr	Glu	Ser	Gln	Leu	Cys	Cys	Gln	Leu	Lys	Leu	Trp	Leu		

130 135 140

Pro Val Gly Cys Ala Ala Phe Val Val Val Leu Leu Phe Gly Cys Ile
145 150 155 160

Leu Ile Ile Trp Phe Ser Lys Lys Lys Tyr Gly Ser Ser Val His Asp
165 170 175

Pro Asn Ser Glu Tyr Met Phe Met Ala Ala Val Asn Thr Asn Lys Lys
180 185 190

Ser Arg Leu Ala Gly Val Thr Ser
195 200

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<400> 3

Met Lys Pro Tyr Phe Cys Arg Val Phe Val Phe Cys Phe Leu Ile Arg
1 5 10 15

Leu Leu Thr Gly Glu Ile Asn Gly Ser Ala Asp His Arg Met Phe Ser
20 25 30

Phe His Asn Gly Gly Val Gln Ile Ser Cys Lys Tyr Pro Glu Thr Val
35 40 45

Gln Gln Leu Lys Met Arg Leu Phe Arg Glu Arg Glu Val Leu Cys Glu
50 55 60

Leu Thr Lys Thr Lys Gly Ser Gly Asn Ala Val Ser Ile Lys Asn Pro
65 70 75 80

Met Leu Cys Leu Tyr His Leu Ser Asn Asn Ser Val Ser Phe Phe Leu
85 90 95

Asn Asn Pro Asp Ser Ser Gln Gly Ser Tyr Tyr Phe Cys Ser Leu Ser
100 105 110

Ile Phe Asp Pro Pro Pro Phe Gln Glu Arg Asn Leu Ser Gly Gly Tyr
115 120 125

Leu His Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Leu Trp Leu
130 135 140

Pro Val Gly Cys Ala Ala Phe Val Val Val Leu Leu Phe Gly Cys Ile
145 150 155 160

Leu Ile Ile Trp Phe Ser Lys Lys Lys Tyr Gly Ser Ser Val His Asp
165 170 175

Pro Asn Ser Glu Tyr Met Phe Met Ala Ala Val Asn Thr Asn Lys Lys
180 185 190

Ser Arg Leu Ala Gly Val Thr Ser
195 200

<210> 4
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Met Thr Leu Arg Leu Leu Phe Leu Ala Leu Asn Phe Phe Ser Val Gln
1 5 10 15

Val Thr Glu Asn Lys Ile Leu Val Lys Gln Ser Pro Leu Leu Val Val
20 25 30

Asp Ser Asn Glu Val Ser Leu Ser Cys Arg Tyr Ser Tyr Asn Leu Leu
35 40 45

Ala Lys Glu Phe Arg Ala Ser Leu Tyr Lys Gly Val Asn Ser Asp Val
50 55 60

Glu Val Cys Val Gly Asn Gly Asn Phe Thr Tyr Gln Pro Gln Phe Arg
65 70 75 80

Ser Asn Ala Glu Phe Asn Cys Asp Gly Asp Phe Asp Asn Glu Thr Val
85 90 95

Thr Phe Arg Leu Trp Asn Leu His Val Asn His Thr Asp Ile Tyr Phe
100 105 110

Cys Lys Ile Glu Phe Met Tyr Pro Pro Pro Tyr Leu Asp Asn Glu Arg
115 120 125

Ser Asn Gly Thr Ile Ile His Ile Lys Glu Lys His Leu Cys His Thr
130 135 140

Gln Ser Ser Pro Lys Leu Phe Trp Ala Leu Val Val Val Ala Gly Val
145 150 155 160

Leu Phe Cys Tyr Gly Leu Leu Val Thr Val Ala Leu Cys Val Ile Trp
165 170 175

Thr Asn Ser Arg Arg Asn Arg Leu Leu Gln Val Thr Thr Met Asn Met
180 185 190

Thr Pro Arg Arg Pro Gly Leu Thr Arg Lys Pro Tyr Gln Pro Tyr Ala
195 200 205

Pro Ala Arg Asp Phe Ala Ala Tyr Arg Pro
210 215

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<213> Artificial sequence

<220>
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<400> 5

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1 5 10 15

Asn Tyr Phe Cys Pro Pro Pro Ser Gly His Ile Glu Leu Cys Lys Leu
20 25 30

Trp Leu Val Phe Leu Leu Leu Ile Trp Pro Arg Ala
35 40

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<222> (1)..(966)

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Met Gln Leu Lys Cys Pro Cys Phe Val Ser Leu Gly Thr Arg Gln Pro
1 5 10 15

ggt tgg aag aag ctc cat gtt tct agc ggg ttc ttt tct ggt ctt ggt 96
Val Trp Lys Lys Leu His Val Ser Ser Gly Phe Phe Ser Gly Leu Gly
20 25 30

ctg ttc ttg ctg ctg ttg agc agc ctc tgt gct gcc tct gca gag act 144
Leu Phe Leu Leu Leu Leu Ser Ser Leu Cys Ala Ala Ser Ala Glu Thr
35 40 45

gaa gtc ggt gca atg gtg ggc agc aat gtg gtg ctc agc tgc att gac 192
Glu Val Gly Ala Met Val Gly Ser Asn Val Val Leu Ser Cys Ile Asp
50 55 60

ccc cac aga cgc cat ttc aac ttg agt ggt ctg tat gtc tat tgg caa 240
Pro His Arg Arg His Phe Asn Leu Ser Gly Leu Tyr Val Tyr Trp Gln

<210> 7
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<212> PRT
<213> Mus musculus

<400> 7

Met Gln Leu Lys Cys Pro Cys Phe Val Ser Leu Gly Thr Arg Gln Pro
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Val Trp Lys Lys Leu His Val Ser Ser Gly Phe Phe Ser Gly Leu Gly
20 25 30

Leu Phe Leu Leu Leu Leu Ser Ser Leu Cys Ala Ala Ser Ala Glu Thr
35 40 45

Glu Val Gly Ala Met Val Gly Ser Asn Val Val Leu Ser Cys Ile Asp
50 55 60

Pro His Arg Arg His Phe Asn Leu Ser Gly Leu Tyr Val Tyr Trp Gln
65 70 75 80

Ile Glu Asn Pro Glu Val Ser Val Thr Tyr Tyr Leu Pro Tyr Lys Ser
85 90 95

Pro Gly Ile Asn Val Asp Ser Ser Tyr Lys Asn Arg Gly His Leu Ser
100 105 110

Leu Asp Ser Met Lys Gln Gly Asn Phe Ser Leu Tyr Leu Lys Asn Val
115 120 125

Thr Pro Gln Asp Thr Gln Glu Phe Thr Cys Arg Val Phe Met Asn Thr
130 135 140

Ala Thr Glu Leu Val Lys Ile Leu Glu Glu Val Val Arg Leu Arg Val
145 150 155 160

Ala Ala Asn Phe Ser Thr Pro Val Ile Ser Thr Ser Asp Ser Ser Asn
165 170 175

Pro Gly Gln Glu Arg Thr Tyr Thr Cys Met Ser Lys Asn Gly Tyr Pro
180 185 190

Glu Pro Asn Leu Tyr Trp Ile Asn Thr Thr Asp Asn Ser Leu Ile Asp
195 200 205

Thr Ala Leu Gln Asn Asn Thr Val Tyr Leu Asn Lys Leu Gly Leu Tyr
210 215 220

Asp Val Ile Ser Thr Leu Arg Leu Pro Trp Thr Ser Arg Gly Asp Val
225 230 235 240

Leu Cys Cys Val Glu Asn Val Ala Leu His Gln Asn Ile Thr Ser Ile
245 250 255

Ser Gln Ala Glu Ser Phe Thr Gly Asn Asn Thr Lys Asn Pro Gln Glu
260 265 270

Thr His Asn Asn Glu Leu Lys Val Leu Val Pro Val Leu Ala Val Leu
275 280 285

Ala Ala Ala Ala Phe Val Ser Phe Ile Ile Tyr Arg Arg Thr Arg Pro
290 295 300

His Arg Ser Tyr Thr Gly Pro Lys Thr Val Gln Leu Glu Leu Thr Asp
305 310 315 320

His Ala

<210> 8
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<212> PRT
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<400> 8

Met Gln Leu Lys Cys Pro Cys Phe Val Ser Leu Gly Thr Arg Gln Pro
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Val Trp Lys Lys Leu His Val Ser Ser Gly Phe Phe Ser Gly Leu Gly
20 25 30

Leu Phe Leu Leu Leu Leu Ser Ser Leu Cys Ala Ala Ser Ala Glu Thr
35 40 45

Glu Val Gly Ala Met Val Gly Ser Asn Val Val Leu Ser Cys Ile Asp
50 55 60

Pro His Arg Arg His Phe Asn Leu Ser Gly Leu Tyr Val Tyr Trp Gln
65 70 75 80

Ile Glu Asn Pro Glu Val Ser Val Thr Tyr Tyr Leu Pro Tyr Lys Ser
85 90 95

Pro Gly Ile Asn Val Asp Ser Ser Tyr Lys Asn Arg Gly His Leu Ser
100 105 110

Leu Asp Ser Met Lys Gln Gly Asn Phe Ser Leu Tyr Leu Lys Asn Val
115 120 125

Thr Pro Gln Asp Thr Gln Glu Phe Thr Cys Arg Val Phe Met Asn Thr
130 135 140

Ala Thr Glu Leu Val Lys Ile Leu Glu Glu Val Val Arg Leu Arg Val
145 150 155 160

Ala Ala Asn Phe Ser Thr Pro Val Ile Ser Thr Ser Asp Ser Ser Asn
165 170 175

Pro Gly Gln Glu Arg Thr Tyr Thr Cys Met Ser Lys Asn Gly Tyr Pro
180 185 190

Glu Pro Asn Leu Tyr Trp Ile Asn Thr Thr Asp Asn Ser Leu Ile Asp
195 200 205

Thr Ala Leu Gln Asn Asn Thr Val Tyr Leu Asn Lys Leu Gly Leu Tyr
210 215 220

Asp Val Ile Ser Thr Leu Arg Leu Pro Trp Thr Ser Arg Gly Asp Val
225 230 235 240

Leu Cys Cys Val Glu Asn Val Ala Leu His Gln Asn Ile Thr Ser Ile
245 250 255

Ser Gln Ala Glu Ser Phe Thr Gly Asn Asn Thr Lys Asn Pro Gln Glu
260 265 270

Thr His Asn Asn Glu Leu Lys Val Leu Val Pro Val Leu Ala Val Leu
275 280 285

Ala Ala Ala Ala Phe Val Ser Phe Ile Ile Tyr Arg Arg Thr Arg Pro
290 295 300

His Arg Ser Tyr Thr Gly Pro Lys Thr Val Gln Leu Glu Leu Thr Asp
305 310 315 320

His Ala

<210> 9
<211> 306
<212> PRT
<213> Mus musculus

<400> 9

Met	Ala	Cys	Asn	Cys	Gln	Leu	Met	Gln	Asp	Thr	Pro	Leu	Leu	Lys	Phe	1	5	10	15
Pro	Cys	Pro	Arg	Leu	Ile	Leu	Leu	Phe	Val	Leu	Leu	Ile	Arg	Leu	Ser	20	25	30	
Gln	Val	Ser	Ser	Asp	Val	Asp	Glu	Gln	Leu	Ser	Lys	Ser	Val	Lys	Asp	35	40	45	
Lys	Val	Leu	Leu	Pro	Cys	Arg	Tyr	Asn	Ser	Pro	His	Glu	Asp	Glu	Ser	50	55	60	
Glu	Asp	Arg	Ile	Tyr	Trp	Gln	Lys	His	Asp	Lys	Val	Val	Leu	Ser	Val	65	70	75	80
Ile	Ala	Gly	Lys	Leu	Lys	Val	Trp	Pro	Glu	Tyr	Lys	Asn	Arg	Thr	Leu	85	90	95	
Tyr	Asp	Asn	Thr	Thr	Tyr	Ser	Leu	Ile	Ile	Leu	Gly	Leu	Val	Leu	Ser	100	105	110	
Asp	Arg	Gly	Thr	Tyr	Ser	Cys	Val	Val	Gln	Lys	Lys	Glu	Arg	Gly	Thr	115	120	125	
Tyr	Glu	Val	Lys	His	Leu	Ala	Leu	Val	Lys	Leu	Ser	Ile	Lys	Ala	Asp	130	135	140	
Phe	Ser	Thr	Pro	Asn	Ile	Thr	Glu	Ser	Gly	Asn	Pro	Ser	Ala	Asp	Thr	145	150	155	160
Lys	Arg	Ile	Thr	Cys	Phe	Ala	Ser	Gly	Gly	Phe	Pro	Lys	Pro	Arg	Phe	165	170	175	
Ser	Trp	Leu	Glu	Asn	Gly	Arg	Glu	Leu	Pro	Gly	Ile	Asn	Thr	Thr	Ile	180	185	190	
Ser	Gln	Asp	Pro	Glu	Ser	Glu	Leu	Tyr	Thr	Ile	Ser	Ser	Gln	Leu	Asp	195	200	205	
Phe	Asn	Thr	Thr	Arg	Asn	His	Thr	Ile	Lys	Cys	Leu	Ile	Lys	Tyr	Gly	210	215	220	
Asp	Ala	His	Val	Ser	Glu	Asp	Phe	Thr	Trp	Glu	Lys	Pro	Pro	Glu	Asp	225	230	235	240
Pro	Pro	Asp	Ser	Lys	Asn	Thr	Leu	Val	Leu	Phe	Gly	Ala	Gly	Phe	Gly	245	250	255	

Ala Val Ile Thr Val Val Val Ile Val Val Ile Ile Lys Cys Phe Cys
260 265 270

Lys His Arg Ser Cys Phe Arg Arg Asn Glu Ala Ser Arg Glu Thr Asn
275 280 285

Asn Ser Leu Thr Phe Gly Pro Glu Glu Ala Leu Ala Glu Gln Thr Val
290 295 300

Phe Leu
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<213> Artificial sequence

<220>
<223> Synthetic

<400> 10

Met Cys Cys Leu Pro Leu Leu Leu Phe Leu Leu Ser Val Val Leu Cys
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His Ser Tyr Trp Gln Val Leu Val Tyr Lys Asn Arg Leu Ser Leu Asp
20 25 30

Cys Val Val Leu Ala Phe Ser Thr Pro Ile Ser Arg Thr Cys Gly Pro
35 40 45

Pro Trp Asn Ile Thr Thr Val Asn Val Val Val Phe Arg Ser Thr Gly
50 55 60

Pro Glu Thr
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<210> 11
<211> 864
<212> DNA
<213> Homo sapiens

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<221> CDS
<222> (1)..(864)

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Met Arg Leu Gly Ser Pro Gly Leu Leu Phe Leu Leu Phe Ser Ser Leu
1 5 10 15

cga gct gat act cag gag aag gaa gtc aga gcg atg gta ggc agc gac 96
Arg Ala Asp Thr Gln Glu Lys Glu Val Arg Ala Met Val Gly Ser Asp
20 25 30

gtg	gag	ctc	agc	tgc	gct	tgc	cct	gaa	gga	agc	cgt	ttt	gat	tta	aat	144
Val	Glu	Leu	Ser	Cys	Ala	Cys	Pro	Glu	Gly	Ser	Arg	Phe	Asp	Leu	Asn	
		35					40					45				
gat	gtt	tac	gta	tat	tgg	caa	acc	agt	gag	tcg	aaa	acc	gtg	gtg	acc	192
Asp	Val	Tyr	Val	Tyr	Trp	Gln	Thr	Ser	Glu	Ser	Lys	Thr	Val	Val	Thr	
	50					55					60					
tac	cac	atc	cca	cag	aac	agc	tcc	ttg	gaa	aac	gtg	gac	agc	cgc	tac	240
Tyr	His	Ile	Pro	Gln	Asn	Ser	Ser	Leu	Glu	Asn	Val	Asp	Ser	Arg	Tyr	
65					70					75					80	
cgg	aac	cga	gcc	ctg	atg	tca	ccg	gcc	ggc	atg	ctg	cgg	ggc	gac	ttc	288
Arg	Asn	Arg	Ala	Leu	Met	Ser	Pro	Ala	Gly	Met	Leu	Arg	Gly	Asp	Phe	
				85					90					95		
tcc	ctg	cgc	ttg	ttc	aac	gtc	acc	ccc	cag	gac	gag	cag	aag	ttt	cac	336
Ser	Leu	Arg	Leu	Phe	Asn	Val	Thr	Pro	Gln	Asp	Glu	Gln	Lys	Phe	His	
			100					105					110			
tgc	ctg	gtg	ttg	agc	caa	tcc	ctg	gga	ttc	cag	gag	gtt	ttg	agc	gtt	384
Cys	Leu	Val	Leu	Ser	Gln	Ser	Leu	Gly	Phe	Gln	Glu	Val	Leu	Ser	Val	
		115					120					125				
gag	gtt	aca	ctg	cat	gtg	gca	gca	aac	ttc	agc	gtg	ccc	gtc	gtc	agc	432
Glu	Val	Thr	Leu	His	Val	Ala	Ala	Asn	Phe	Ser	Val	Pro	Val	Val	Ser	
	130					135					140					
gcc	ccc	cac	agc	ccc	tcc	cag	gat	gag	ctc	acc	ttc	acg	tgt	aca	tcc	480
Ala	Pro	His	Ser	Pro	Ser	Gln	Asp	Glu	Leu	Thr	Phe	Thr	Cys	Thr	Ser	
145					150					155					160	
ata	aac	ggc	tac	ccc	agg	ccc	aac	gtg	tac	tgg	atc	aat	aag	acg	gac	528
Ile	Asn	Gly	Tyr	Pro	Arg	Pro	Asn	Val	Tyr	Trp	Ile	Asn	Lys	Thr	Asp	
				165					170				175			
aac	agc	ctg	ctg	gac	cag	gct	ctg	cag	aat	gac	acc	gtc	ttc	ttg	aac	576
Asn	Ser	Leu	Leu	Asp	Gln	Ala	Leu	Gln	Asn	Asp	Thr	Val	Phe	Leu	Asn	
			180					185					190			
atg	cgg	ggc	ttg	tat	gac	gtg	gtc	agc	gtg	ctg	agg	atc	gca	cgg	acc	624
Met	Arg	Gly	Leu	Tyr	Asp	Val	Val	Ser	Val	Leu	Arg	Ile	Ala	Arg	Thr	
		195					200					205				
ccc	agc	gtg	aac	att	ggc	tgc	tgc	ata	gag	aac	gtg	ctt	ctg	cag	cag	672
Pro	Ser	Val	Asn	Ile	Gly	Cys	Cys	Ile	Glu	Asn	Val	Leu	Leu	Gln	Gln	
	210					215					220					
aac	ctg	act	gtc	ggc	agc	cag	aca	gga	aat	gac	atc	gga	gag	aga	gac	720
Asn	Leu	Thr	Val	Gly	Ser	Gln	Thr	Gly	Asn	Asp	Ile	Gly	Glu	Arg	Asp	
225					230					235					240	
aag	atc	aca	gag	aat	cca	gtc	agt	acc	ggc	gag	aaa	aac	gcg	gcc	acg	768
Lys	Ile	Thr	Glu	Asn	Pro	Val	Ser	Thr	Gly	Glu	Lys	Asn	Ala	Ala	Thr	
				245					250					255		
tgg	agc	atc	ctg	gct	gtc	ctg	tgc	ctg	ctt	gtg	gtc	gtg	gcg	gtg	gcc	816
Trp	Ser	Ile	Leu	Ala	Val	Leu	Cys	Leu	Leu	Val	Val	Val	Ala	Val	Ala	
			260				265						270			
ata	ggc	tgg	gtg	tgc	agg	gac	cga	tgc	ctc	caa	cac	agc	tat	gca	ggc	864
Ile	Gly	Trp	Val	Cys	Arg	Asp	Arg	Cys	Leu	Gln	His	Ser	Tyr	Ala	Gly	
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<210> 12
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<212> PRT
<213> Homo sapiens

<400> 12

Met Arg Leu Gly Ser Pro Gly Leu Leu Phe Leu Leu Phe Ser Ser Leu
1 5 10 15

Arg Ala Asp Thr Gln Glu Lys Glu Val Arg Ala Met Val Gly Ser Asp
20 25 30

Val Glu Leu Ser Cys Ala Cys Pro Glu Gly Ser Arg Phe Asp Leu Asn
35 40 45

Asp Val Tyr Val Tyr Trp Gln Thr Ser Glu Ser Lys Thr Val Val Thr
50 55 60

Tyr His Ile Pro Gln Asn Ser Ser Leu Glu Asn Val Asp Ser Arg Tyr
65 70 75 80

Arg Asn Arg Ala Leu Met Ser Pro Ala Gly Met Leu Arg Gly Asp Phe
85 90 95

Ser Leu Arg Leu Phe Asn Val Thr Pro Gln Asp Glu Gln Lys Phe His
100 105 110

Cys Leu Val Leu Ser Gln Ser Leu Gly Phe Gln Glu Val Leu Ser Val
115 120 125

Glu Val Thr Leu His Val Ala Ala Asn Phe Ser Val Pro Val Val Ser
130 135 140

Ala Pro His Ser Pro Ser Gln Asp Glu Leu Thr Phe Thr Cys Thr Ser
145 150 155 160

Ile Asn Gly Tyr Pro Arg Pro Asn Val Tyr Trp Ile Asn Lys Thr Asp
165 170 175

Asn Ser Leu Leu Asp Gln Ala Leu Gln Asn Asp Thr Val Phe Leu Asn
180 185 190

Met Arg Gly Leu Tyr Asp Val Val Ser Val Leu Arg Ile Ala Arg Thr
195 200 205

Pro Ser Val Asn Ile Gly Cys Cys Ile Glu Asn Val Leu Leu Gln Gln
210 215 220

Asn Leu Thr Val Gly Ser Gln Thr Gly Asn Asp Ile Gly Glu Arg Asp
225 230 235 240

Lys Ile Thr Glu Asn Pro Val Ser Thr Gly Glu Lys Asn Ala Ala Thr
245 250 255

Trp Ser Ile Leu Ala Val Leu Cys Leu Leu Val Val Val Ala Val Ala
260 265 270

Ile Gly Trp Val Cys Arg Asp Arg Cys Leu Gln His Ser Tyr Ala Gly
275 280 285

<210> 13
<211> 267
<212> PRT
<213> Homo sapiens

<400> 13

Glu Lys Glu Val Arg Ala Met Val Gly Ser Asp Val Glu Leu Ser Cys
1 5 10 15

Ala Cys Pro Glu Gly Ser Arg Phe Asp Leu Asn Asp Val Tyr Val Tyr
20 25 30

Trp Gln Thr Ser Glu Ser Lys Thr Val Val Thr Tyr His Ile Pro Gln
35 40 45

Asn Ser Ser Leu Glu Asn Val Asp Ser Arg Tyr Arg Asn Arg Ala Leu
50 55 60

Met Ser Pro Ala Gly Met Leu Arg Gly Asp Phe Ser Leu Arg Leu Phe
65 70 75 80

Asn Val Thr Pro Gln Asp Glu Gln Lys Phe His Cys Leu Val Leu Ser
85 90 95

Gln Ser Leu Gly Phe Gln Glu Val Leu Ser Val Glu Val Thr Leu His
100 105 110

Val Ala Ala Asn Phe Ser Val Pro Val Val Ser Ala Pro His Ser Pro
115 120 125

Ser Gln Asp Glu Leu Thr Phe Thr Cys Thr Ser Ile Asn Gly Tyr Pro
130 135 140

Arg Pro Asn Val Tyr Trp Ile Asn Lys Thr Asp Asn Ser Leu Leu Asp
145 150 155 160

Gln Ala Leu Gln Asn Asp Thr Val Phe Leu Asn Met Arg Gly Leu Tyr
165 170 175

Asp Val Val Ser Val Leu Arg Ile Ala Arg Thr Pro Ser Val Asn Ile
180 185 190

Gly Cys Cys Ile Glu Asn Val Leu Leu Gln Gln Asn Leu Thr Val Gly
195 200 205

Ser Gln Thr Gly Asn Asp Ile Gly Glu Arg Asp Lys Ile Thr Glu Asn
210 215 220

Pro Val Ser Thr Gly Glu Lys Asn Ala Ala Thr Trp Ser Ile Leu Ala
225 230 235 240

Val Leu Cys Leu Leu Val Val Val Ala Val Ala Ile Gly Trp Val Cys
245 250 255

Arg Asp Arg Cys Leu Gln His Ser Tyr Ala Gly
260 265

<210> 14
<211> 276
<212> PRT
<213> Mus musculus

<400> 14

Glu Thr Glu Val Gly Ala Met Val Gly Ser Asn Val Val Leu Ser Cys
1 5 10 15

Ile Asp Pro His Arg Arg His Phe Asn Leu Ser Gly Leu Tyr Val Tyr
20 25 30

Trp Gln Ile Glu Asn Pro Glu Val Ser Val Thr Tyr Tyr Leu Pro Tyr
35 40 45

Lys Ser Pro Gly Ile Asn Val Asp Ser Ser Tyr Lys Asn Arg Gly His
50 55 60

Leu Ser Leu Asp Ser Met Lys Gln Gly Asn Phe Ser Leu Tyr Leu Lys
65 70 75 80

Asn Val Thr Pro Gln Asp Thr Gln Glu Phe Thr Cys Arg Val Phe Met
85 90 95

Asn Thr Ala Thr Glu Leu Val Lys Ile Leu Glu Glu Val Val Arg Leu
100 105 110

Arg Val Ala Ala Asn Phe Ser Thr Pro Val Ile Ser Thr Ser Asp Ser

115		120		125
Ser Asn Pro Gly Gln Glu Arg Thr Tyr Thr Cys Met Ser Lys Asn Gly				
130		135		140
Tyr Pro Glu Pro Asn Leu Tyr Trp Ile Asn Thr Thr Asp Asn Ser Leu				
145		150		155
Ile Asp Thr Ala Leu Gln Asn Asn Thr Val Tyr Leu Asn Lys Leu Gly				
	165		170	175
Leu Tyr Asp Val Ile Ser Thr Leu Arg Leu Pro Trp Thr Ser Arg Gly				
	180		185	190
Asp Val Leu Cys Cys Val Glu Asn Val Ala Leu His Gln Asn Ile Thr				
	195		200	205
Ser Ile Ser Gln Ala Glu Ser Phe Thr Gly Asn Asn Thr Lys Asn Pro				
210		215		220
Gln Glu Thr His Asn Asn Glu Leu Lys Val Leu Val Pro Val Leu Ala				
225		230		235
Val Leu Ala Ala Ala Ala Phe Val Ser Phe Ile Ile Tyr Arg Arg Thr				
	245		250	255
Arg Pro His Arg Ser Tyr Thr Gly Pro Lys Thr Val Gln Leu Glu Leu				
	260		265	270
Thr Asp His Ala				
	275			

<210> 15
 <211> 125
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Synthetic

<400> 15

Glu Glu Val Ala Met Val Gly Ser Val Leu Ser Cys Pro Phe Leu Tyr
1 5 10 15
Val Tyr Trp Gln Val Thr Tyr Pro Ser Asn Val Asp Ser Tyr Asn Arg
20 25 30
Ser Met Gly Phe Ser Leu Leu Asn Val Thr Pro Gln Asp Gln Phe Cys
35 40 45

Val Leu Val Leu Val Ala Ala Asn Phe Ser Pro Val Ser Ser Glu Thr
50 55 60

Thr Cys Ser Asn Gly Tyr Pro Pro Asn Tyr Trp Ile Asn Thr Asp Asn
65 70 75 80

Ser Leu Asp Ala Leu Gln Asn Thr Val Leu Asn Gly Leu Tyr Asp Val
85 90 95

Ser Leu Arg Thr Cys Cys Glu Asn Val Leu Gln Asn Thr Ser Gln Gly
100 105 110

Lys Lys Leu Ala Val Leu Val Ile Arg Arg Ser Tyr Gly
115 120 125

<210> 16
<211> 1294
<212> DNA
<213> Homo sapiens

<220>
<221> 5'UTR
<222> (1)..(199)

<220>
<221> CDS
<222> (200)..(1105)

<400> 16
gctggtacgc ctgcaggtac cggctcggaa ttcccgggtc gacccacgcg tccgcccacg 60
cgctccgcggg agcgcagtta gagccgatct cccgcgcccc gaggttgctc ctctccgagg 120
tctcccgcgg cccaagttct ccgcgccccg aggtctccgc gccccgaggt ctccgcggcc 180
cgaggtctcc gcccgacc atg cgg ctg ggc agt cct gga ctg ctc ttc ctg 232
Met Arg Leu Gly Ser Pro Gly Leu Leu Phe Leu
1 5 10
ctc ttc agc agc ctt cga gct gat act cag gag aag gaa gtc aga gcg 280
Leu Phe Ser Ser Leu Arg Ala Asp Thr Gln Glu Lys Glu Val Arg Ala
15 20 25
atg gta ggc agc gac gtg gag ctc agc tgc gct tgc cct gaa gga agc 328
Met Val Gly Ser Asp Val Glu Leu Ser Cys Ala Cys Pro Glu Gly Ser
30 35 40
cgt ttt gat tta aat gat gtt tac gta tat tgg caa acc agt gag tcg 376
Arg Phe Asp Leu Asn Asp Val Tyr Val Tyr Trp Gln Thr Ser Glu Ser
45 50 55
aaa acc gtg gtg acc tac cac atc cca cag aac agc tcc ttg gaa aac 424
Lys Thr Val Val Thr Tyr His Ile Pro Gln Asn Ser Ser Leu Glu Asn
60 65 70 75
gtg gac agc cgc tac cgg aac cga gcc ctg atg tca ccg gcc ggc atg 472
Val Asp Ser Arg Tyr Arg Asn Arg Ala Leu Met Ser Pro Ala Gly Met

<210> 17
<211> 302
<212> PRT
<213> Homo sapiens

<400> 17

Met Arg Leu Gly Ser Pro Gly Leu Leu Phe Leu Leu Phe Ser Ser Leu
1 5 10 15

Arg Ala Asp Thr Gln Glu Lys Glu Val Arg Ala Met Val Gly Ser Asp
20 25 30

Val Glu Leu Ser Cys Ala Cys Pro Glu Gly Ser Arg Phe Asp Leu Asn
35 40 45

Asp Val Tyr Val Tyr Trp Gln Thr Ser Glu Ser Lys Thr Val Val Thr
50 55 60

Tyr His Ile Pro Gln Asn Ser Ser Leu Glu Asn Val Asp Ser Arg Tyr
65 70 75 80

Arg Asn Arg Ala Leu Met Ser Pro Ala Gly Met Leu Arg Gly Asp Phe
85 90 95

Ser Leu Arg Leu Phe Asn Val Thr Pro Gln Asp Glu Gln Lys Phe His
100 105 110

Cys Leu Val Leu Ser Gln Ser Leu Gly Phe Gln Glu Val Leu Ser Val
115 120 125

Glu Val Thr Leu His Val Ala Ala Asn Phe Ser Val Pro Val Val Ser
130 135 140

Ala Pro His Ser Pro Ser Gln Asp Glu Leu Thr Phe Thr Cys Thr Ser
145 150 155 160

Ile Asn Gly Tyr Pro Arg Pro Asn Val Tyr Trp Ile Asn Lys Thr Asp
165 170 175

Asn Ser Leu Leu Asp Gln Ala Leu Gln Asn Asp Thr Val Phe Leu Asn
180 185 190

Met Arg Gly Leu Tyr Asp Val Val Ser Val Leu Arg Ile Ala Arg Thr
195 200 205

Pro Ser Val Asn Ile Gly Cys Cys Ile Glu Asn Val Leu Leu Gln Gln
210 215 220

Asn Leu Thr Val Gly Ser Gln Thr Gly Asn Asp Ile Gly Glu Arg Asp
225 230 235 240

Lys Ile Thr Glu Asn Pro Val Ser Thr Gly Glu Lys Asn Ala Ala Thr
245 250 255

Trp Ser Ile Leu Ala Val Leu Cys Leu Leu Val Val Val Ala Val Ala
260 265 270

Ile Gly Trp Val Cys Arg Asp Arg Cys Leu Gln His Ser Tyr Ala Gly
275 280 285

Ala Trp Ala Val Ser Pro Glu Thr Glu Leu Thr Gly His Val
290 295 300

<210> 18
<211> 302
<212> PRT
<213> Homo sapiens

<400> 18

Met Arg Leu Gly Ser Pro Gly Leu Leu Phe Leu Leu Phe Ser Ser Leu
1 5 10 15

Arg Ala Asp Thr Gln Glu Lys Glu Val Arg Ala Met Val Gly Ser Asp
20 25 30

Val Glu Leu Ser Cys Ala Cys Pro Glu Gly Ser Arg Phe Asp Leu Asn
35 40 45

Asp Val Tyr Val Tyr Trp Gln Thr Ser Glu Ser Lys Thr Val Val Thr
50 55 60

Tyr His Ile Pro Gln Asn Ser Ser Leu Glu Asn Val Asp Ser Arg Tyr
65 70 75 80

Arg Asn Arg Ala Leu Met Ser Pro Ala Gly Met Leu Arg Gly Asp Phe
85 90 95

Ser Leu Arg Leu Phe Asn Val Thr Pro Gln Asp Glu Gln Lys Phe His
100 105 110

Cys Leu Val Leu Ser Gln Ser Leu Gly Phe Gln Glu Val Leu Ser Val
115 120 125

Glu Val Thr Leu His Val Ala Ala Asn Phe Ser Val Pro Val Val Ser
130 135 140

Ala Pro His Ser Pro Ser Gln Asp Glu Leu Thr Phe Thr Cys Thr Ser

145		150		155		160
Ile Asn Gly Tyr	Pro Arg Pro Asn Val Tyr	Trp Ile Asn Lys Thr Asp				
	165	170				175
Asn Ser Leu Leu	Asp Gln Ala Leu Gln Asn Asp Thr Val Phe Leu Asn					
	180	185				190
Met Arg Gly Leu Tyr Asp Val Val Ser Val Leu Arg Ile Ala Arg Thr						
	195	200				205
Pro Ser Val Asn Ile Gly Cys Cys Ile Glu Asn Val Leu Leu Gln Gln						
	210	215				220
Asn Leu Thr Val Gly Ser Gln Thr Gly Asn Asp Ile Gly Glu Arg Asp						
	225	230				235
Lys Ile Thr Glu Asn Pro Val Ser Thr Gly Glu Lys Asn Ala Ala Thr						
	245	250				255
Trp Ser Ile Leu Ala Val Leu Cys Leu Leu Val Val Val Ala Val Ala						
	260	265				270
Ile Gly Trp Val Cys Arg Asp Arg Cys Leu Gln His Ser Tyr Ala Gly						
	275	280				285
Ala Trp Ala Val Ser Pro Glu Thr Glu Leu Thr Gly His Val						
	290	295				300
<210> 19						
<211> 322						
<212> PRT						
<213> Mus musculus						
<400> 19						
Met Gln Leu Lys Cys Pro Cys Phe Val Ser Leu Gly Thr Arg Gln Pro						
1	5	10				15
Val Trp Lys Lys Leu His Val Ser Ser Gly Phe Phe Ser Gly Leu Gly						
	20	25				30
Leu Phe Leu Leu Leu Leu Ser Ser Leu Cys Ala Ala Ser Ala Glu Thr						
	35	40				45
Glu Val Gly Ala Met Val Gly Ser Asn Val Val Leu Ser Cys Ile Asp						
	50	55				60
Pro His Arg Arg His Phe Asn Leu Ser Gly Leu Tyr Val Tyr Trp Gln						
65	70	75				80

Ile Glu Asn Pro Glu Val Ser Val Thr Tyr Tyr Leu Pro Tyr Lys Ser
85 90 95

Pro Gly Ile Asn Val Asp Ser Ser Tyr Lys Asn Arg Gly His Leu Ser
100 105 110

Leu Asp Ser Met Lys Gln Gly Asn Phe Ser Leu Tyr Leu Lys Asn Val
115 120 125

Thr Pro Gln Asp Thr Gln Glu Phe Thr Cys Arg Val Phe Met Asn Thr
130 135 140

Ala Thr Glu Leu Val Lys Ile Leu Glu Glu Val Val Arg Leu Arg Val
145 150 155 160

Ala Ala Asn Phe Ser Thr Pro Val Ile Ser Thr Ser Asp Ser Ser Asn
165 170 175

Pro Gly Gln Glu Arg Thr Tyr Thr Cys Met Ser Lys Asn Gly Tyr Pro
180 185 190

Glu Pro Asn Leu Tyr Trp Ile Asn Thr Thr Asp Asn Ser Leu Ile Asp
195 200 205

Thr Ala Leu Gln Asn Asn Thr Val Tyr Leu Asn Lys Leu Gly Leu Tyr
210 215 220

Asp Val Ile Ser Thr Leu Arg Leu Pro Trp Thr Ser Arg Gly Asp Val
225 230 235 240

Leu Cys Cys Val Glu Asn Val Ala Leu His Gln Asn Ile Thr Ser Ile
245 250 255

Ser Gln Ala Glu Ser Phe Thr Gly Asn Asn Thr Lys Asn Pro Gln Glu
260 265 270

Thr His Asn Asn Glu Leu Lys Val Leu Val Pro Val Leu Ala Val Leu
275 280 285

Ala Ala Ala Ala Phe Val Ser Phe Ile Ile Tyr Arg Arg Thr Arg Pro
290 295 300

His Arg Ser Tyr Thr Gly Pro Lys Thr Val Gln Leu Glu Leu Thr Asp
305 310 315 320

His Ala

<210> 20
 <211> 143
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Synthetic

<400> 20

Met Leu Pro Gly Leu Leu Phe Leu Leu Ser Ser Leu Ala Glu Glu Val
 1 5 10 15

Ala Met Val Gly Ser Val Leu Ser Cys Pro Phe Leu Tyr Val Tyr Trp
 20 25 30

Gln Val Thr Tyr Pro Ser Asn Val Asp Ser Tyr Asn Arg Ser Met Gly
 35 40 45

Phe Ser Leu Leu Asn Val Thr Pro Gln Asp Gln Phe Cys Val Leu Val
 50 55 60

Leu Val Ala Ala Asn Phe Ser Pro Val Ser Ser Glu Thr Thr Cys Ser
 65 70 75 80

Asn Gly Tyr Pro Pro Asn Tyr Trp Ile Asn Thr Asp Asn Ser Leu Asp
 85 90 95

Ala Leu Gln Asn Thr Val Leu Asn Gly Leu Tyr Asp Val Ser Leu Arg
 100 105 110

Thr Cys Cys Glu Asn Val Leu Gln Asn Thr Ser Gln Gly Lys Lys Leu
 115 120 125

Ala Val Leu Val Ile Arg Arg Ser Tyr Gly Val Glu Leu Thr His
 130 135 140

<210> 21
 <211> 1370
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> (1)..(165)

<220>
 <221> CDS
 <222> (166)..(762)

<400> 21
 aacaatttca cacaggaaac agctatgacc atgattacgc caagctctaa tacgactcac 60

tatagggaaa gctggtacgc ctgcaggtac cgggtccggaa ttcccggggtc gacccacgcg	120
tccgtgaaca ctgaacgcga ggactgttaa ctgtttctgg caaac atg aag tca ggc	177
Met Lys Ser Gly	
1	
ctc tgg tat ttc ttt ctc ttc tgc ttg cgc att aaa gtt tta aca gga	225
Leu Trp Tyr Phe Phe Leu Phe Cys Leu Arg Ile Lys Val Leu Thr Gly	
5 10 15 20	
gaa atc aat ggt tct gcc aat tat gag atg ttt ata ttt cac aac gga	273
Glu Ile Asn Gly Ser Ala Asn Tyr Glu Met Phe Ile Phe His Asn Gly	
25 30 35	
ggt gta caa att tta tgc aaa tat cct gac att gtc cag caa ttt aaa	321
Gly Val Gln Ile Leu Cys Lys Tyr Pro Asp Ile Val Gln Gln Phe Lys	
40 45 50	
atg cag ttg ctg aaa ggg ggg caa ata ctc tgc gat ctc act aag aca	369
Met Gln Leu Leu Lys Gly Gly Gln Ile Leu Cys Asp Leu Thr Lys Thr	
55 60 65	
aaa gga agt gga aac aca gtg tcc att aag agt ctg aaa ttc tgc cat	417
Lys Gly Ser Gly Asn Thr Val Ser Ile Lys Ser Leu Lys Phe Cys His	
70 75 80	
tct cag tta tcc aac aac agt gtc tct ttt ttt cta tac aac ttg gac	465
Ser Gln Leu Ser Asn Asn Ser Val Ser Phe Phe Leu Tyr Asn Leu Asp	
85 90 95 100	
cat tct cat gcc aac tat tac ttc tgc aac cta tca att ttt gat cct	513
His Ser His Ala Asn Tyr Tyr Phe Cys Asn Leu Ser Ile Phe Asp Pro	
105 110 115	
cct cct ttt aaa gta act ctt aca gga gga tat ttg cat att tat gaa	561
Pro Pro Phe Lys Val Thr Leu Thr Gly Gly Tyr Leu His Ile Tyr Glu	
120 125 130	
tca caa ctt tgt tgc cag ctg aag ttc tgg tta ccc ata gga tgt gca	609
Ser Gln Leu Cys Cys Gln Leu Lys Phe Trp Leu Pro Ile Gly Cys Ala	
135 140 145	
gcc ttt gtt gta gtc tgc att ttg gga tgc ata ctt att tgt tgg ctt	657
Ala Phe Val Val Val Cys Ile Leu Gly Cys Ile Leu Ile Cys Trp Leu	
150 155 160	
aca aaa aag aag tat tca tcc agt gtg cac gac cct aac ggt gaa tac	705
Thr Lys Lys Lys Tyr Ser Ser Ser Val His Asp Pro Asn Gly Glu Tyr	
165 170 175 180	
atg ttc atg aga gca gtg aac aca gcc aaa aaa tct aga ctc aca gat	753
Met Phe Met Arg Ala Val Asn Thr Ala Lys Lys Ser Arg Leu Thr Asp	
185 190 195	
gtg acc cta taatatggaa ctctggcacc caggcatgaa gcacgttggc	802
Val Thr Leu	
cagtttttcc caacttgaag tgcaagattc tcttatttcc gggaccacgg agagtctgac	862
ttactacat acatcttctg ctgggtgtttt gttcaatctg gaagaatgac tgtatcagtc	922
aatgggggatt ttaacagact gccttggtac tgccgagtc tctcaaaaca aacaccctct	982

tgcaaccagc tttggagaaa gccagctcc tgtgtgctca ctgggagtgg aatccctgtc 1042
 tccacatctg ctctagcag tgcacagcc agtaaaacaa acacatttac aagaaaaatg 1102
 ttttaaagat gccaggggta ctgaatctgc aaagcaaag agcagccaag gaccagcatc 1162
 tgtccgcatt tcactatcat actacctctt ctttctgtag ggatgagaat tcctctttta 1222
 atcagtcaag ggagatgctt caaagctgga gctattttat ttctgagatg ttgatgtgaa 1282
 ctgtacatta gtacatactc agtactctcc ttcaattgct gaaccccagt tgaccatttt 1342
 accaagactt tagatgcttt cttgtgcc 1370

<210> 22
 <211> 199
 <212> PRT
 <213> Homo sapiens

<400> 22

Met Lys Ser Gly Leu Trp Tyr Phe Phe Leu Phe Cys Leu Arg Ile Lys
 1 5 10 15

Val Leu Thr Gly Glu Ile Asn Gly Ser Ala Asn Tyr Glu Met Phe Ile
 20 25 30

Phe His Asn Gly Gly Val Gln Ile Leu Cys Lys Tyr Pro Asp Ile Val
 35 40 45

Gln Gln Phe Lys Met Gln Leu Leu Lys Gly Gly Gln Ile Leu Cys Asp
 50 55 60

Leu Thr Lys Thr Lys Gly Ser Gly Asn Thr Val Ser Ile Lys Ser Leu
 65 70 75 80

Lys Phe Cys His Ser Gln Leu Ser Asn Asn Ser Val Ser Phe Phe Leu
 85 90 95

Tyr Asn Leu Asp His Ser His Ala Asn Tyr Tyr Phe Cys Asn Leu Ser
 100 105 110

Ile Phe Asp Pro Pro Pro Phe Lys Val Thr Leu Thr Gly Gly Tyr Leu
 115 120 125

His Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Phe Trp Leu Pro
 130 135 140

Ile Gly Cys Ala Ala Phe Val Val Val Cys Ile Leu Gly Cys Ile Leu
 145 150 155 160

Ile Cys Trp Leu Thr Lys Lys Lys Tyr Ser Ser Ser Val His Asp Pro

	165		170		175
Asn Gly Glu Tyr Met Phe Met Arg Ala Val Asn Thr Ala Lys Lys Ser	180		185		190
Arg Leu Thr Asp Val Thr Leu	195				
<210> 23					
<211> 199					
<212> PRT					
<213> Homo sapiens					
<400> 23					
Met Lys Ser Gly Leu Trp Tyr Phe Phe Leu Phe Cys Leu Arg Ile Lys	1	5	10		15
Val Leu Thr Gly Glu Ile Asn Gly Ser Ala Asn Tyr Glu Met Phe Ile	20		25		30
Phe His Asn Gly Gly Val Gln Ile Leu Cys Lys Tyr Pro Asp Ile Val	35		40		45
Gln Gln Phe Lys Met Gln Leu Leu Lys Gly Gly Gln Ile Leu Cys Asp	50		55		60
Leu Thr Lys Thr Lys Gly Ser Gly Asn Thr Val Ser Ile Lys Ser Leu	65		70		75
Lys Phe Cys His Ser Gln Leu Ser Asn Asn Ser Val Ser Phe Phe Leu	85		90		95
Tyr Asn Leu Asp His Ser His Ala Asn Tyr Tyr Phe Cys Asn Leu Ser	100		105		110
Ile Phe Asp Pro Pro Pro Phe Lys Val Thr Leu Thr Gly Gly Tyr Leu	115		120		125
His Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Phe Trp Leu Pro	130		135		140
Ile Gly Cys Ala Ala Phe Val Val Val Cys Ile Leu Gly Cys Ile Leu	145		150		155
Ile Cys Trp Leu Thr Lys Lys Lys Tyr Ser Ser Ser Val His Asp Pro	165		170		175
Asn Gly Glu Tyr Met Phe Met Arg Ala Val Asn Thr Ala Lys Lys Ser	180		185		190

Arg Leu Thr Asp Val Thr Leu
195

<210> 24
<211> 200
<212> PRT
<213> Mus musculus

<400> 24

Met Lys Pro Tyr Phe Cys Arg Val Phe Val Phe Cys Phe Leu Ile Arg
1 5 10 15

Leu Leu Thr Gly Glu Ile Asn Gly Ser Ala Asp His Arg Met Phe Ser
20 25 30

Phe His Asn Gly Gly Val Gln Ile Ser Cys Lys Tyr Pro Glu Thr Val
35 40 45

Gln Gln Leu Lys Met Arg Leu Phe Arg Glu Arg Glu Val Leu Cys Glu
50 55 60

Leu Thr Lys Thr Lys Gly Ser Gly Asn Ala Val Ser Ile Lys Asn Pro
65 70 75 80

Met Leu Cys Leu Tyr His Leu Ser Asn Asn Ser Val Ser Phe Phe Leu
85 90 95

Asn Asn Pro Asp Ser Ser Gln Gly Ser Tyr Tyr Phe Cys Ser Leu Ser
100 105 110

Ile Phe Asp Pro Pro Pro Phe Gln Glu Arg Asn Leu Ser Gly Gly Tyr
115 120 125

Leu His Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Leu Trp Leu
130 135 140

Pro Val Gly Cys Ala Ala Phe Val Val Val Leu Leu Phe Gly Cys Ile
145 150 155 160

Leu Ile Ile Trp Phe Ser Lys Lys Lys Tyr Gly Ser Ser Val His Asp
165 170 175

Pro Asn Ser Glu Tyr Met Phe Met Ala Ala Val Asn Thr Asn Lys Lys
180 185 190

Ser Arg Leu Ala Gly Val Thr Ser
195 200

<210> 25
<211> 24
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oglionucleotide

<400> 25
accatgcggc tgggcagtcg tgga 24

<210> 26
<211> 23
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oglionucleotide

<400> 26
tggtgacctc ccacatccca cag 23

<210> 27
<211> 23
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oglionucleotide

<400> 27
tccgatgtca tttcctgtct ggc 23

<210> 28
<211> 24
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oglionucleotide

<400> 28
gctctgtctc cggactcaca gccc 24

<210> 29
<211> 28
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oglionucleotide

<400> 29
gtggcagcaa acttcagcgt gcccgctcg 28

<210> 30
<211> 28
<212> DNA

<213> Artificial sequence
<220>
<223> Synthetic oglionucleotide
<400> 30
cccaacgtgt actggatcaa taagacgg 28

<210> 31
<211> 28
<212> DNA
<213> Artificial sequence
<220>
<223> Synthetic oglionucleotide
<400> 31
gcgtgctgag gatcgacgg acccccag 28

<210> 32
<211> 21
<212> DNA
<213> Artificial sequence
<220>
<223> Synthetic oglionucleotide
<400> 32
gcctctagaa agagctggga c 21

<210> 33
<211> 21
<212> DNA
<213> Artificial sequence
<220>
<223> Synthetic oglionucleotide
<400> 33
cgccgtgttc catttatgag c 21

<210> 34
<211> 18
<212> DNA
<213> Artificial sequence
<220>
<223> Synthetic oglionucleotide
<400> 34
gcatatttat gaatccca 18

<210> 35
<211> 18
<212> DNA
<213> Artificial sequence
<220>
<223> Synthetic oglionucleotide

<400> 35
actattaggg tcatgcac

18

<210> 36
<211> 6
<212> PRT
<213> Artificial sequence

<220>
<223> Motif

<400> 36

Phe Asp Pro Pro Pro Phe
1 5

<210> 37
<211> 6
<212> PRT
<213> Artificial sequence

<220>
<223> Motif

<400> 37

Met Tyr Pro Pro Pro Tyr
1 5